Input file ftmzb48h10; Output File ftmzb48h10.pat
Sequence length 3637

GTC	GACC	CACC	CCTC	cccz	CTC	ACAP	ATGCC	TGC	сстс	тстс	SACTO	CAC	CGTC	cccc	ccc	CTG	cccc	ccc	GCGCC	79
CAA	GCCA	AGTO	GAGO	GGGG	GCG1	TGCC	CACC	GACC	GCAC	AGCC	CTTC	GGC	CCGC	CCGGC	SACCA	AGGA	GTG/	AGCC	GCGCG	158
CGC	ACAG	CTCC	GTGC	GCTC	GCCC	GTCT	GAGC	GCCC	GCCA	GGTG	ecco	GCAC	ccc	cccc	CGAC	M ATC	H CAC	S AGC	P CCG	4 233
P CCT	_	L CTC	L CTG	A GCG	L CTG	W TGG	L CTT	C TGC	A GCT	V GTG	L CTG	C TGC	A GC#		A GCG	R CGC	G GGG	G GGC	S AGC	24 293
D GAC	_	Q CAG	P CCT	G GGC	P CCG	G GGG	R CGT	P CCC		C TGC	P CCG	A GCT	CCC	C TGC	H CAC	C TGC	Q CAG	E GAG	D GAC	44 353
G GGC		M ATG	L CTG	S TCC	A GCT	D GAC	C TGC	S TCC	E GAG	L CTC	G GGG	L CTC	S TCA	V GTG	V GTG	P CCT	A GCG	D GAC	L CTG	64 413
D GAC	P CCC	L CTG	T ACG	A GCT	Y TAC			L CTC	S AGT	M ATG	N AAC	N AAC	L CTC	T ACG	E GAG	L CTT	Q CAG	P CCG	G GGT	84 473
L CTC	_			L CTG	R CGC	F TTC	L CTG	E GAG	E GAG	L CTG	R CGG	L CTC	S TCA	G GGG	N AAC	H CAC	L CTC	S TCA	H CAC	104 533
•	P CCG		Q CAG	A GCA	F TTC		G GGC	L CTC	H CAC	,	L CTC		I ATT		~ M ATG	L CTG	Q CAG	S AGC	N AAC	124 593
Q CAG	L CTC	R CGT	G GGG	I ATC	P CCA	A GCA	E GAG	A GCA	L CTA	W TGG	E GAG	L CTG	P CCC	S AGC	L CTG	Q CAG	S TCG	L CTG	R CGC	144 653
L	D	A	N	L	I	s	L	v	P CCT	E	R	s	F	E	G	L	s	s	L	164 713
R CGC	H CAC	L CTC	w TGG	L CTG	D GAT	D GAC	N AAT		L CTC	T ACT	E GAG	I ATC	P CCC	V GTC	R AGA	A GCT	L CTC	N AAC	N AAC	184 773
L	P	A	L	Q	A	М	T	L	A GCT	L	N	н	I	R	н	I	P	D	Y	204 833
A	F	Q	N	L	T	s	L	v	V GTG	L	н	L	н	N	N	R	ı.	Q	н	224 893
v	G	T	н	s	F	E	G	L	H CAC	N	L	E	T	L	D	L	N	Y	N	244 953
E	 L	Q	E	F	P	L	A	I	R	T	L	G	R	L	Q	E	L	G	F	264 1013
н	N	N	N	I	к	A	ı	P	E	ĸ	A	F	M	G	N	P	L	L	Q	284 1073
T	I	Н	F	Y	D	N	P	I	Q CAG	F	v	G	R	s	A	F	Q	Y	L	304 1133
s	ĸ	L	н	T	L	s	L	N	G	A	T	D	I	Q	E	F	P	Đ	L	324 1193
K	G	Т	т	s	L	E	I	L	т	L	т	R	A	G	I	R	L	L	P	344 1253

Figure 1

I L S E R L R L н CCG GGA GTG TGC CAA CAG CTG CCT AGG CTC CGA ATC CTG GAG CTG TCT CAT AAT CAG ATC С Q K L E Н R E I G 384 GAG GAG TTA CCC AGC CTG CAC AGA TGT CAG AAG CTG GAG GAA ATT GGC CTC CGA CAT AAC 1373 S Q E I G А D Т F S L G L 404 AGG ATC AAG GAA ATT GGT GCA GAT ACC TTC AGC CAG CTG GGC TCC TTG CAA GCT TTA GAC R A I H P E A F S T L R S 424 CTG AGT TGG AAT GCC ATC CGT GCC ATC CAC CCT GAG GCT TTC TCA ACC CTT CGA TCC TTG D N Q L т т P L 444 GTT AAG CTG GAC CTG ACT GAC AAC CAG CTG ACC ACA CTG CCC CTG GCT GGG CTG GGA GGC 1553 LKGNLALS 0 A 464 CTG ATG CAC CTG AAG CTC AAA GGG AAC TTG GCC CTG TCT CAG GCC TTC TCC AAG GAC AGT R ILE v P Y A Y Q 484 TTC CCA AAA CTG AGG ATC CTG GAG GTG CCC TAC GCC TAC CAG TGC TGT GCC TAC GGC ATC 1673 K Т S G Q+ W А E D F 0 H TGT GCC AGC TTC TTC AAG ACC TCT GGG CAG TGG CAG GCC GAG GAC TTT CAT CCA GAA GAA P L G L L A G Q A ~E 524 GAG GAG GCA CCA AAG AGG CCC CTG GGT CTC CTT GCT GGA CAA GCT GAG AAC CAC TAT GAC 0 М G Т E D K P s N CTA GAC CTG GAT GAG CTC CAG ATG GGG ACA GAG GAC TCA AAG CCA AAC CCC AGT GTC CAG v G P F K P С E Н L 564 TGC AGC CCT GTT CCA GGC CCC TTC AAG CCC TGC GAG CAC CTC TTT GAG AGC TGG GGC ATC 1913 S C А Ι L L L N G L 584 CGC CTT GCT GTG TGG GCC ATC GTG CTC TCC GTA CTC TGT AAC GGG CTG GTG CTG A S G P S P L S P V K 604 ACA GTC TTT GCC AGC GGA CCC AGC CCG CTG TCC CCC GTC AAG CTT GTG GTG GGT GCG ATG 2033 TGISCGLLA 624 GCA GGC GCC AAC GCC CTG ACG GGC ATT TCC TGT GGT CTC CTG GCC TCT GTG GAC GCC TTG 2093 A E Y G A R W E S G L ACC TAT GGT CAG TTC GCT GAG TAT GGA GCC CGC TGG GAG AGC GGT CTG GGC TGC CAG GCT E S L L 664 ACG GGC TTC CTG GCT GTC CTG GGT TCA GAG GCG TCG GTG CTG CTC ACA CTG GCG GCC T C R A Y G ĸ GTG CAG TGC AGC ATC TCT GTG ACC TGC GTC CGA GCC TAC GGG AAG GCG CCG TCG CCT GGC 2273 С G L Α L Α G L Α A 704 AGC GTC CGC GCA GGC GCA CTG GGA TGC CTG GCG CTG GCC GGG CTG GCC GCA GCA CTG CCG 2333 G Y E G А S L L 724 CTG GCC TCG GTG GGA GAG TAT GGC GCC TCC CCA CTC TGC CTG CCC TAC GCC CCA CCC GAG G Α V A L V M M N S L С 744 GGC CGG CCG GCC CTG GGC TTC GCT GTA GCC CTG GTG ATG ATG AAC TCG CTC TGC TTC 2453

Figure 1 (Cont'd)

L CTG	V GTG	V GTG	A GCC	G GGC	A GCC	Y TAC	I ATC	K : AAG	L CTC	Y TAC	C TG:	D GAO	L CTC	P CCF	R CGG	G GG:	D GAO	ŢŢ.	E GAG	76 251
A	V	W	D	_			V													78
GCC	GIG	166	GAC	. 160	. GCC	ATG	GIG	CGC	CAC	GIG	GCC	: 1G0	Cre	ATC	111	· GC	A GAT	r GGC	CTC	257
		C TGC					L CTC		F TTT						L CTC			V GTC	T ACC	80 263
		A					L										L	N	P	824
ccc	GAG	GCT	GTC	AAG	TCA	GTC	CTT	CTG	GTG	GTG	CTG	CCT	CTG	CCT	GCC	TGC	CTC	AAC	CCA	2693
L	L	Y	L	L	F	N	P	н	F	R	D			R	R	L	W	P	s	844
CTG	CTC	TAC	CTG	CTC	TTC	AAC	CCT	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CGG	CTC	TGG	CCA	AGC	2753
							A GCC							L CTG		K AAG	S AGC	S TCC	C TGC	864 2813
	S TCC		Q CAA		L CTG		GCT	TTC	TCA	D GAT	V GTG	D GAT	CTT	I ATT	L CTG	E GAA	A GCT	S TCT	E GAG	884 2873
A		-			G		E					P		v		L		s	R	904
GCT	GGG	CAG	CCT	CCT	GGG	CTA	GAG	ACC	TAT	GGC	TTC	CCT	TCA	GTG	ACC	CTC	ATC	TCC	CGA	2933
H	Q	P	G	A	T	R	L					F				D		T		924
CAT	CAG	CCG	GGG	GCC	ACC	AGG	CTG	GAG	GGA	AAC	CAT	TTT	ATA	GAG	TCT	GAT	GGA	ACC	AAG	2993
					P		M	ĸ	G	E	L	· L	L	ĸ	A	E	G.	A		944
TTT	GGG	AAC	CCA	CAA	CCT	CCC	ATG	AAG	GGA	GAA	CTG	CTG	CTG	AAG	GCA	GAG	GGA	GCC	ACT	3053
L TTG							V GTG												A GCC	964 3113
S TCT	H CAC	L TTG '	± TAA																	968 3125
ATAT	CCCT	CTCT	GTTT	GTCC	тстс	CCCA	TCCA	ATGA'	TGGC	IGCT	TATA	AAAG	AAAG	ACAA	crcc	AACT	CCAT	AGCA	Aga	3204
TGGC	CAAC	ACCT	CTGA	CTCC	ATTG	TTCT	CTCT	CCAC	GACC	CCTA	ACCA	ATGA	GTGC	TTCC	aagt	CTTG	CTTT	GTCT	rg g	3283
CCTT	CAGC	TTCA	CTTT	CACC	CTGG	GCCT	TCTC	IGTC	CAAT	CCAA	TACT	TCTG	ACAG.	AGGC	CTGG	GAAA	TTTG	CATA	GGA	3362
GAAA	GGAG	AAAA	GCAA	AAGA	CAGT	gaag	GTTA:	TTGG	3CCC	rgac:	agag	CCAT	GATC	AGTA	AGTG	CAGA	GTGA	TGGG	GAG	3441
GTCT	CACA	GAGCI	ATGA	CACT	GGAA	GACA	ACTA	CCAA	AGAC	ATTG	GAGA	GTCT	cccc	rgtg/	ACAT	atag.	AATA	TAAA	ATG	3520
IGTT	CTGC	STTC	CATT	AATC	TTGA	CCTA	TGCT	GNGC	CAAA	FIGC	TTCC	TGTT.	AAAA'	TACA	TTT	GGAA(GACA'	TTGA	AAA	3599
AAAA	AAAA	LAAA	AAAA	AAAA	AAAA	AAAA	GGGC	GCC(3C											3637

Figure 1 (Cont'd)

```
LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10
           *->nLeeLdLsnNkLtsippgalsnLpnLeeLdLsnNnLtsippgifqnLk<-*
             +LdLs N+Lt+I pg++++L+ LeeL Ls+N+L+++p ++f++L+
  ftmzb048h1
          67 LTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH 114
LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08
          *->nLeeLdLsnNkLtsippgalsnLpnLeeLdLsnNnLtsippglfqnLk<-*
            +L+ L L+ N+L+++p++a|+ Lp+L++L L+ N ++ +p+++f++L+
 ftmzb048h1
      115 SLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS 162
LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11
          *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
            +L++L+L++N Lt++p al+nLp L+ L N++++p+++fqnL+
 ftmzb048h1
      163 SLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLT 210
LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08
          *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL k<-*
           +L +L+L nN+++++ +++++L+nLe+LdL++N+L+++p + + L+ _
 ftmzb048h1
      211 SLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFPL-AIRTLG 257
LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06
          *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfgnLk<-*
           +L+eL + nN+++ +p+ a+ + p L+++++ +N ++ + ++fq L+
 ftmzb048h1
     258 RLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLS 305
LRR: domain 6 of 8, from 306 to 352; score 23.8, E = 0.0041
         *->nLeeLdLsnNk.LtslppgalsnLpnLeeLdLsnNnLtslppglfqn Lk<-*
           +L++L+L++ +++++p+ I++ ++Le L L + ++ Ippg++q L+
 ftmzb048h1
     306 KLHTLSLNGATdIQEFPD-LKGTTSLEILTLTRAGIRLLPPGVCQQLP 352
LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10
          *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
           +L+ L+Ls+N++++|p+ |+ +++Lee+ L +N+++++ ++f+ L+
ftmzb048h1
      353 RLRILELSHNQIEELPS-LHRCQKLEEIGLRHNRIKEIGADTFSQLG 398
LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11
          *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
           +L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+ip ++L
ftmzb048h1
       399 SLQALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLM 446
```

Figure 2

Proteins with leucine-rich repeats

Protein (species)*	Function-ligand*	Locational	Repeats	Length	Concons	US 60	que	noe"				PIR' entr
				1	. 5	10		15	20	2	5	 -
RNase inhibitor (porcine)	RNase inhibitor-RNase	Cytoplasm	15	28 (A)	.LE.L.L							A31857
Laurence de la comp			_	29 (B)	.L.EL.L							
Leucine-rich @2-GP (human)	7–7	Serum	8	24	.LL.L							NBHUA2
RNA1 (Saccharomyces cerevisiae)		Cytopiasm	8	29	.LL.L							BVBYN1
U2 snRNP A' (human)	Splicing-U2 snRNP	Nucleus	4	24	.LL.a							S03616
Biglycan (human)	ECM binding-laminin, fibronectin, TGFβ	ECM	8	24	.LL.L	N-	. I	a	a		•	A40757
Decorin (human)	ECM binding-collagen, fibronectin, thrombospondin, TGF-β	ECM	10	24	.LL.L	N	. I	v	a		• •	NBHUC8
Fibromodulin (bovine)	ECM binding-collagen, fibronectin	ECM	11	24	.LL.L	.N	a	-a	a	. .	•	S05390
Lumican (chicken)	Comeal transparency-?	ECM	12	24	.LL.L.	.N	L		a			A41748
Proteoglycan-Lb (chicken)	7-7	ECM	6	24	.La.L.							A41781
Osteoinductive factor (bovine)	Bone morphogenesis-BMP	ECM	6	24	.La.L.							A35272
Platelet GP log (human)	Cell adhesion-vWF, thrombin	PM (EC)	7	24	.LL.L.							NBHUIA
Platelet GP V (human)	Cell adhesion-GP IX, GP Ib	PM (EC)	14	24	.LL.L.							HOHOM.
YopM (Yersinia pestis)	Virulence factor-thrombin	IC + EC	12	20	.LL.a.							A33950
pal-17.8 (Shigella flexneri)	7-7	?	6	20	.LL.V.							A35149
pal-14.5 (Shigetia flexneri)	7-7	?	8	20	.LL.a.							
Toll (Drosophila)	Embryo development-?	PM (EC)	19	24	.LL.L.							\$18248
SRt (Drosophila)	Axon development-?	EC EC	19									A29943
Connectin (Drosophila)	Synapse development-?	PM (EC)	7	24	.LL.L.					-		A36665
Chaoptin (<i>Drosophil</i> a)			30	24 24	.LLNL.							S28464
Rightiess-I (Drosophila)	Photoreceptor-cell development-?				.LL.L.							A29944
	Embryo development-?	PM (EC)		23	.LL.LS							-
Digodendrocyte myelin GP (human)	Myelination-?	PM (EC)	-	24	.LL.LS 	NN; •	a	-a	L	, .		A34210
2014 (human)	Cell-surface receptor-LPS-LPB	PM (EC)			.aL.L.	. N						TDHUM4
irk (human)	Receptor protein kinase-NGF	PM (EC)	2	23	.LL.LS	. N I	ما	:				TVHUTT
rkB (mouse)	Receptor protein kinase-BDNF, NT-3	PM (EC)	3	23	.LL.aT	. N I	LTS.	· · · - ·		T		S06943
irkC (porcine)	Receptor protein kinase-NT-3	PM (EC)	3	23	. LR . aNILS	N1	١	.s		-		A40026
MK1 (Arabidopsis thaliana)	Receptor protein kinase-?	PM (EC)	11	23	.La.L.	.N	G.	.aP	-a.SL	, .		J01674
H-CG receptor (rat)	Signal transduction-LH, CG	PM (EC)	5	25	.LL.a.	T	1 .		.F			A41343
SH receptor (rat)	Signal transduction-FSH	PM (EC)	7	25	.LL.aS	T		LP	.aa			A34548
SH receptor (dog)	Signal transduction-TSH	PM (EC)	6 :	25	.aL.a.l	₽ ĕ	s.S-	-a	.a			A40077
denylate cyclase (Saccharomyces	Signal transduction-RAS	PM .	20		.LL.L.							OYBY.
cerevisiae)	_	(cytoplasm)										
LR (Trypanosoma brucel)	7–7	?```	18 :	23	.LL.LS	x2	١	-a	-aL	 .		A36359
AD1 (Saccharomyces cerevisiae)	DNA repair-RAD10	Nucleus			a.LaDI.							DDBYD1
AD7 (Saccharomyces cerevisiae)	DNA repair-?	?		==	L.L.a.							A25226
RT100 (Arabidopsis thaliana)	Recombination-?	Chloroplast			L.LNL.					_		A46260
RR1 (Saccharomyces cerevisiae)	Signal transduction-?	Cytoolasm			L.a.L.							A41529
CR4 (Saccharomyces cerevisiae)	Transcription-?	?			LL.a.							S31286
ds22 (Schlzosaccharomyces pombel	Mitosis-dis2, sds21	Nucleus		==	LL.a.							A38439
34 ribosome-binding protein (rat)	RM membranes-ribosome	RM membrane (cytoplasm)	4	24	.LLDL.	N I	-	LP	.FL	-		-
arbogypeptidase N (human)	Stabilization-catalytic subunit	Plasma	12 :	24	.LL.L.	N- 1		I.D.	AF I			A34901
itemalin (Listeria monocytogenes)	Invasion-?	Cell wall		= -	LL.L.							A39930
NB (Listeria monocytogenes)	?-?	?			LL.L.	NI	DI	- -	-LL			C39930
RR superfamily					5 .LL.L.		-		0 25			

Figure 3

>human DNA seg. TAATACGACTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAA TTCCCGGGTCGACCCACGCGTCCGTGGAGCCGAGCCAGGGTCTGAGCCTGCC GGCTCATCCAGCCTCTTGCTGCCCTAGCGGCCTCCAACACCACCGCATCTG GGAAATTGGAGCT:GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATC TTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCAC TCCCTGGTCAAGCTGGACCTGACAGCAGCTGACCACACTGCCCCTGGC TGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCCC AGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATG CCTACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCC CCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATG AGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAGC CCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCAT CCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGG TGCTGCTGACCGTGTTCGCTGGCGGGCCTGCCCCCTGCCCCGGTCAAGTTT GTGGTAGGTGCGATTGCAGGCGCCAACACCTTGACTGGCATTTCCTGTGGCCT TCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCC GCTGGGAGACGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGG GTCGGAGGCATCGGTGCTGCTCACTCTGGCCGCAGTGCAGTGCAGCGTC AGCAGGGGTCCTAGGCTGCCTGGCACTGCCAGGGCTGGCCGCACTGCCC CACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAT GAACTCCTTCTGTTTCCTGGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGA CCTGCCGCGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCT CAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGT CTGTCCTGCTGGTGCTGCCCCCTGCCTGCCTCAACCCACTGCTGTAC CTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGCGGGCTTCGGCCCCGCGC AGGGGACTCAGGCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGC TCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTG GAAGCTTCTGAAGCTGGGCGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC AGTGACCCTCATCTCCTGTCAGCAGCCAGGGCCCCCAGGCTGGAGGGCAGC CATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCTCCATGGA TGGAGAACTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTG TCAGGGGGTGGCGCTTTCAGCCCTCTGGCTTTGGCCTTTGCTTCACACGTGTA AATATCCCTCCCCATTCTTCTCTTCCCCTCTCTCCCCTCG GTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCT CACCAACGGGTGCCTCTGGCCTTCCCTTGGCCTTCCCCAGCTTCACCT TGATACTGGGCCTCTTCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGAC TTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGG TTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGT GATTTCCCGTGTGACTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAT CTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATT GCATGCGACGTCATAGCTCTTCTATAGTGTCACCTAAATTCAATT

Figure 4

>fahr human

NTTHYRESWYACRYRSGIPGSTHASVERSQGLSLPAHPASLAALAASNTTASGKLE DTFSQLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHL KLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDLHLD DEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYL FESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCG LLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSEASVLLLTLAAVQCSVSVS CVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQP AALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFAD GLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLR RLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYG FPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL SGGGGFQPSGLAFASHV

LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11

*->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL
+L+ LdLs N ++s++p+a+s+L++L +LdL +N+Lt+lp + +L
fahr 64 SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGL 110

k<-*

fahr 111 M 111

Etweh048h10	l Mespecilalmicavicasabogs	1100W3W3W9&CP&DC96CTFCC	THE SADOSEL GLSVVEADL	08 Stringgeratykanist
As of sambbooldil2		Dt Dt ot and a street of a		
Cahr human				
	81		~ ^^~ns way \$507 DOT ^CT D	160
Etmzb048h10	TOPGER PLANTAGE AND A STREET	TROUN SCHOOL TO THE	INCTENTION STATISTICS	Weary 200 LEGGE STATE
Az_of_sembb001d112				
fahr_human	161			240
ftmzb048h10	LSSLRHIMIDDNALTHIPVRALM	LPALONITEALNICERHIEPDYA	FORT.TSIAVIATEMENTOH	VCTHSFEGLHNLETED
Az_of_aambb001d112				
fahr human				
	241		•	320
£tmzb048h10	LNYNELQEFPLAIRTLCRLQELCE	hdavika i pekafacanti (7	TYOPKENDY QUENCHING	SQIATI-SINGATDIQE
As_of_aambb001d112				
fakr Jaman	***************************************		MHYRES	
	321			400
ftmzb048b10	PPOLEGYTSLETT/TLTRAGIRLLE	BOACCONTRUCTS SHIPOTE	STAPSTARE OF TREATMENT	KITKKICKDERSÖNGER
As of ambb001d112			······································	
Eahr_Imman .	HASVERSQCLSLI	ARPASLAALAASNITAS	X3	DTFSQLSSL 460
	401 QALIKSKRIATRATKIPEAFSTERSI		MATERIAL SOLVENS	
funzh048h10	CALLESMATRATHPEAPSTERST		MILKURICKI ALSOAFSKOS	
Na_of_sambb001d112	ONLOLSHNAIRSTHPEAFSTLHSI			
fahr_human	481			560
5	AYGIĆASFFKTSGQWQAEDFHPER	PPAPKRPI GIJAGOAFNHYDI	DEDECTION OF THE SERVICE OF THE SERV	CSPVPGPFKPCEHLFE
ftmzb046h10 Aa_of_aambb001d112	AYGICASFFATSGONQAEDFHPE	EPAPKRPLGLLAGOAENED/DL	DEDEL CHOTEDSKPHPSVQ	CSPVPGPPKPCEHLFE
fabr_baman	PYCHCASFFXASQUEAEDERILE	PESSKRPIGLIARQAENHYD)	OLDET (CLEMEDSKEHRSVQ	CSPTPGPFKPCEYLFE
1,5 T	561	·		640
ftesb048h10	SECURIAVEATVIJSVICNCIVIJ	TVFA9GPSPLSPVKI.VVGAHA	CANALIGISCOLLASVDAL	TYGQFAEYGARWESGL
As of sambboold112	SHEIRLAVIRIVILLSVLCHEAVLI	TVFA::GPSPLSPVKLVVGAMA	LATVERLECELLECELLARIES	TYGOFAEYGARORSGL
Enhr Jumon	SHCIRLAWATVILSVIONGWIA			
	641		MI	720
Eczeb048h10	GCONTGELAVIGSEASVILLTIA	WCS18VICVRAYCAAPSRGS	AMENING TWINKER WATER	LASVGERGASHALLARI
As of south001d112	CCONTGELAVICESEASVILLITLAV GCRATGELAVICESEASVILLITLAV	VQCSISVICVKAIGKAESEC	TARA DALLATAN MANAGEME	Kaskerkaspinia.
Estate James		ACSASASCALATARSESIN		
8	721 TM 11		VIMT	800
£t=zb048h10	APPEGREAALGEAVALWRESSLCI	TAWAGAYIKI MCDK PRGDEE	NVKDCMKVRHVAKLIFADGE	Lycivaficeachici.
As of ambb001d112	APPROPRATORAVALUMOSIC	LVVAGAYIKLYCDLPRGDEZ	NA EDCIMENTALIZATION DE LA COMPANION DE LA COM	LYCPVAFISFASMICE
fahr human	APPRICEARLGETVALVANCESEC	LVVAGAYTKLYCDLPRGDFE	NAMOCAMARHAMILITATICE	TACHARISMANIA.
i = i	801 771		7	MAT 880
ftmsb048b10	FPVFPPRVKSVLUVLPLPACIA	ALYLLENDHUR HOLKRUMPS	Prspgplayaargeleksso	DSTOALWAFEDVOLIL
Acof_aambb001d112	PPVIPENVESVILAVLEI PACIE	MAYILENPHERDU ARIAPS	Prspgplayaaagelekss	DSTQUENTSDVILLE
fahr Juman	PPVTPEAVKSVILLVVLPLPACIA		NGDGGPLAYAAAGEL2855	
	881 TM	NT ·		0 3 @
ftmzb048h10	EASEAGOPPGLETYGPPSVTLIS	RHORCATRIZERIP I ESDOTA	FGNPUPPHKISELLAKARSHI	ia rouceerineri mad Mandozaddirine 20
Aa_of_aambb001d112	EASENGOPPGLETYGFPSVTLIS EASENGRPFGLETYGFPSVTLIS	KGETK TEUT BOARDE HIMERAGE KGETK TEUT TEUT BEFLA KESTYALY	ECHTAL CONTRACTOR AND	CONTRACTOR DESCRIPTION
fahr_human	_	Market Strategy of A Sharket	ANTAL MANAGEMENT (ARTON)	968
	961 G ENGEN			
ftmzb048b10	SLFASRLN SLFASRLN			
Aa_of_aanbb001d112 fahr human	LAFASEVN			

Figure 7

20 K N Y , N Т D L L GGG CTG CAC AAT CTG GAG ACA CTA GAC CTG AAT TAT AAC AAG CTG CAG GAG TTC CCT GTG 60 F N N N Ι 40 G Н Q E L GCC ATC CGG ACC CTG GGC AGA CTG CAG GAA CTG GGG TTC CAT AAC AAC AAC ATC AAG GCC 120 60 Q Т Т Н F Y G N Ρ L L Α F М K ATC CCA GAA AAG GCC TTC ATG GGG AAC CCT CTG CTA CAG ACG ATA CAC TTT TAT GAT AAC 180 80 S s Α F 0 Y Ρ K \mathbf{L} Н Т R G CCA ATC CAG TTT GTG GGA AGA TCG GCA TTC CAG TAC CTG CCT AAA CTC CAC ACA CTA TCT 240 100 G F Ρ D L K D Ι Q Ε CTG AAT GGT GCC ATG GAC ATC CAG GAG TTT CCA GAT CTC AAA GGC ACC ACC AGC CTG GAG 300 S G 120 P М G Ι R L L ATC CTG ACC CTG ACC CGC GCA GGC ATC CGG CTG CTC CCA TCG GGG ATG TGC CAA CAG CTG 360 140 Е E T, V L S Н N Q Ι R Ε L R R L R V L E L S H N Q I E E L P S L H CCC AGG CTC CGA GTC CTG GAA CTG TCT CAC AAT CAA ATT GAG GAG CTG CCC AGC CTG CAC 160 Õ Н N R Ι W Ι G Ε ÁGG TGT CAG AAA TTG GAG GAA ATC GGC CTC CAA CAC AAC CGC ATC TGG GAA ATT GGA GCT 480 180 T F S S S L 0 Α L D L S W N Q L GAC ACC TTC AGC CAG CTG AGC TCC CTG CAA GCC CTG GAT CTT AGC TGG AAC GCC ATC CGG 540 200 S T Н S K S I H P E A F S T L H S L V K L D L T D
TCC ATC CAC CCT GAG GCC TTC TCC ACC CTG CAC TCC CTG GTC AAG CTG GAC CTG ACA GAC F L 600 220 G L G G L М Т Т P Τ. Α L L AAC CAG CTG ACC ACA CTG CCC CTG GCT GGA CTT GGG GGC TTG ATG CAT CTG AAG CTC AAA 660 240 K D S F S Q Α GGG AAC CTT GCT CTC TCC CAG GCC TTC TCC AAG GAC AGT TTC CCA AAA CTG AGG ATC CTG 720 260 С С Ρ Y G М С Α Y Α Y 0 GAG GTG CCT TAT GCC TAC CAG TGC TGT CCC TAT GGG ATG TGT GCC AGC TTC TTC AAG GCC 780 Е 280 D D F. L Ε D L Н TCT GGG CAG TGG GAG GCT GAA GAC CTT CAC CTT GAT GAT GAG GAG TCT TCA AAA AGG CCC 840 300 E Y D Q D L D Q Α Ν Н L Α R L CTG GGC CTC CTT GCC AGA CAA GCA GAG AAC CAC TAT GAC CAG GAC CTG GAT GAG CTC CAG 900 320 С v Q S М E D S K Р Η ₽ S CTG GAG ATG GAG GAC TCA AAG CCA CAC CCC AGT GTC CAG TGT AGC CCT ACT CCA GGC CCC 960 340 v W А S W G Ι R \mathbf{L} Α Р Y L F Ε С E TTC AAG CCC TGT GAG TAC CTC TTT GAA AGC TGG GGC ATC CGC CTG GCC GTG TGG GCC ATC 1020 360 C Ν G L \mathbf{L} GTG TTG CTC TCC GTG CTC TGC AAT GGA CTG GTG CTG CTG ACC GTG TTC GCT GGC GGG CCT 1080 380 G Α Ν L F V V G A Ι Α Р Р v K GCC CCC CTG CCC CCG GTC AAG TTT GTG GTA GGT GCG ATT GCA GGC GCC AAC ACC TTG ACT 1140

FIGURE 8

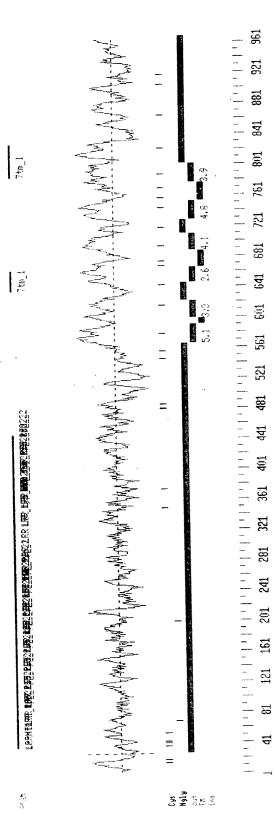
G GGC	I ATT	S TCC	C TGT	G GGC	L	L CTA	A GCC	S TCA	V GTC	D GAT	A GCC	L CTG		F TTT	G GGT	Q CAG	F TTC	S TCT	E GAG	400 1200
Y	G	A	R	W	E	T	G	L	G	C	R	A	T		F	L	A	V	L	420
TAC	GGA	GCC	CGC	TGG	GAG	ACG	GGG	CTA	GGC	TGC	CGG	GCC	ACT		TTC	CTG	GCA	GTA	CTT	1260
G	S	E	A	S	V	L	L	L	T	L	A		V	Q	C	S	V	S	V	440
GGG	TCG	GAG	GCA	TCG	GTG	CTG	CTG	CTC	ACT	CTG	GCC		GTG	CAG	TGC	AGC	GTC	TCC	GTC	1320
S	C	V	R	A	Y	G	K	S	P	S	L	G	S	V	R	A	G	V	L	460
TCC	TGT	GTC	CGG	GCC	TAT	GGG	AAG	TCC	CCC	TCC	CTG	GGC	AGC	GTT	CGA	GCA	GGG	GTC	CTA	1380
G GGC	C TGC	L CTG	A GCA	L CTG	A GCA	G GGG	L CTG	A GCC	A GCC	A GCA	L CTG	P		A GCC	S TCA	V GTG	G GGA	E GAA	Y TAC	480 1440
G	A	S	P	L	C	L	P	Y TAC	A	P	P	E	G	Q	P	A	A	L	G	500
GGG	GCC	TCC	CCA	CTC	TGC	CTG	CCC		GCG	CCA	CCT	GAG	GGT	CAG	CCA	GCA	GCC	CTG	GGC	1500
F	T	V	A	L	V	M	M	N	S	F	C	F	L	V	V	A	G	A	Y	520
TTC	ACC	GTG	GCC	CTG	GTG	ATG	ATG	AAC	TCC	TTC	TGT	TTC	CTG	GTC	GTG	GCC	GGT	GCC	TAC	1560
1122	K AAA	L CTG	Y TAC	C TGT	D GAC	L CTG	P CCG	R CGG	GGC	D GAC	F TTT	E GAG	A GCC	V GTG	W TGG	D GAC	C TGC	A GCC	M ATG	540 1620
Y	R	H	V	A	W	L CTC	I	F	A	D	G	L	L	Y	C	P	V	A	F	560
GTG	AGG	CAC	GTG	GCC	TGG		ATC	TTC	GCA	GAC	GGG	CTC	CTC	TAC	TGT	CCC	GTG	GCC	TTC	1680
H	S	F	A	.S	M	L	G	L	F	P	V	T	CCC	E	A	V	K	S	V	580
Grc	AGC	TTC	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACG		GAG	GCC	GTC	AAG	TCT	GTC	1740
L	L	V	V	L	P	L	P	A	C	L	N	P		L	Y	L	L	F	N	600
CTG	CTG	GTG	GTG	CTG	CCC	CTG	CCT	GCC	TGC	CTC	AAC	CCA		CTG	TAC	CTG	CTC	TTC	AAC	1800
P	H	F	R	D	D	L	R	R	L	R	P	R	A	G	D	S	G	P	L	620
CCC	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CGG	CTT	CGG	CCC	CGC	GCA	GGG	GAC	TCA	GGG	CCC	CTA	1860
A	Y	A	A	A	G	E	L	E	K	S	S	C	D	S	T	Q	A	L	V	640
GCC	TAT	GCT	GCG	GCC	GGG	GAG	CTG	GAG	AAG	AGC	TCC	TGT	GAT	TCT	ACC	CAG	GCC	CTG	GTA	1920
A	F	S	D	V	D	L	I	L	E	A	S	E	A	G	R	CCC	P	G	L	660
GCC	TTC	TCT	GAT	GTG	GAT	CTC	ATT	CTG	GAA	GCT	TCT	GAA	GCT	GGG	CGG		CCT	GGG	CTG	1980
E	T	Y	G	F	P	S	V	T	L	I	S	C	Q	Q	P	G	A	CCC	R	680
GAG	ACC	TAT	GGC	TTC	CCC	TCA	GTG	ACC	CTC	ATC	TCC	TGT	CAG	CAG	CCA	GGG	GCC		AGG	2 04 0
L CTG	E GAG	G GGC	S AGC	H CAT	C TGT	V GTA	E GAG	P CCA	E GAG	G GGG	N AAC	H CAC	F TTT	G GGG	N AAC	CCC	Q CAA	P	S TCC	700 2 10 0
M	D	G	E	L	L	L	R	A	E	G	S	T	P	A	G	G	G	L	S	720
ATG	GAT	GGA	GAA	CTG	CTG	CTG	AGG	GCA	GAG	GGA	TCT	ACG	CCA	GCA	GGT	GGA	GGC	TTG	TCA	2160
G GGG	G GGT	G GGC	G GGC	F TTT	Q CAG	P CCC	S TCT	G GGC	L TTG	A GCC	F TTT	A GCT	S TCA	H CAC	V G T G	* TAA				737 2211
ATA	TCCC	TCCC	CATI	CTTC	тстт	cccc	CTCTC	TTCC	сттт	CCTC	TCTC	cccc	TCGG	TGAA	TGAT	GGCI	GCTT	CTAA	AACA	2290
AATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAGTACCTGGCTGG												2369								
CCATCACCAACGGGTGCCTCTGGCCTTGGCCTTGGCCTTCGTCAGGTTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTT												2448								
TCA	TGTC	TGAA	AGCTO	STGG <i>F</i>	ACCAC	GAGAC	CCTGC	SACTI	TTGT	CTGC	TTAF	AGGGA	TAAL	SAGGO	SAAGI	CAAAC	SACAG	TGA	AGGGG	2527

CONT.

TGGAAGAGATTAAAAAAAAAAAAAA	2711
GATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTT	2685
TGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGTGATTTCCCGTGTGACTCATG	2606

FIGURE 8 CONT.

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Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
                 /prod/ddm/seqanal/PFAM/pfam6.2/Pfam
                  /prod/ddm/wspace/orfanal/oa-script.12184.seq
Sequence file:
Query: 15088
Scores for sequence family classification (score includes all domains):
                                     Score E-value N
Model Description
                                                1.3e-68 16
       Leucine Rich Repeat
                                         241.4
LRRNT Leucine rich repeat N-terminal domain 7 transmembrane receptor (rhodopsin family)
                                                 27.2 0.00038 1
                                                         0.14 2
                                                 7.2
Parsed for domains:
Model Domain seq-f seq-t hmm-f hmm-t score E-value
                34 65 .. 1 31 [] 27.2 0.00038
LRRNT
              67 90 .. 1 23 [] 12.4
91 114 .. 1 23 [] 24.2
                                           11
LRR
        1/16
                                   24.2 0.0031
LRR
        2/16
              115 138 .. 1 23 [] 19.9 0.062
LRR
        3/16
              139 162 ..
                              23 []
                                    16.4
                                           0.7
LRR
        4/16
                           1
LRR
              163 186 ..
                              23 fl
                                    27.5 0.00031
        5/16
LRR
        6/16
              187 210 ..
                          1 23 []
                                    12.1
                                            13
              211 234 ..
                              23 []
                                    21.6
                                          0.019
LRR
        7/16
              235 257...
                              23 []
                                    18.2
                                           0.2
LRR
        8/16
                                    19.0
                                           0.11
LRR
              258 281 ..
                           1 23 []
        9/16
LRR
        10/16
              282 305 ..
                           1
                              23 []
                                    10.2
                                             32
        11/16
              306 328 ..
LRR
                              23 []
                                     5.6 1.5e+02
               329 352 ..
                                     8.8
LRR
        12/16
                              23 []
                                            52
                           1
                                     19.2
                                           0.097
LRR
        13/16
               353 374 ..
                            1
                              23 []
        14/16
              375 398 .. 1 23 []
                                    16.9
                                            0.49
LRR
LRR
              399 422 ..
                           1 23 []
                                     23.7 0.0042
        15/16
                           1 23 []
                                    16.4
        16/16 423 446 ..
                                           0.66
LRR
              635 662 .. 51 79 ..
7tm 1
        1/2
                                     3.4
                                           2.2
7tm_1
        2/2
              784 827.. 207 259.]
                                      1.1
Alignments of top-scoring domains:
LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038
          *->aCpreCtCsp..fglvVdCsgrgLtlevPrdlP<-*
            aCp++C+C +++ I+ dCs++gL +vP dl
    15088 34 ACPAPCHCQEdgIMLSADCSELGLS-AVPGDLD 65
LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11
          *->nLeeLdLsnN.LtslppglfsnLp<-*
             +LdLs N+Lt+l pglf++L+
    15088 67 LTAYLDLSMNnLTELQPGLFHHLR 90
LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031
          *->nLeeLdLsnN.LtslppglfsnLp<-*
            LeeL+Ls+N+L+++p +fs+L
    15088 91 FLEELRLSGNhLSHIPGQAFSGLY 114
LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062
           *->nLeeLdLsnN.LtslppglfsnLp<-*
    +L+ L L+nN+L ++p +++ Lp
15088 115 SLKILMLQNNqLGGIPAEALWELP 138
LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7
           *->nLeeLdLsnN.LtslppglfsnLp<-*
            +L++L+L+ N ++ +p+ +f++L+
    15088 139 SLQSLRLDANIISLVPERSFEGLS 162
LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031
           *->nLeeLdLsnN.LtslppglfsnLp<-*
```

+L++L+L++N Lt++p +++nLp

FIGURE 10

15088 163 SLRHLWLDDNaLTEIPVRALNNLP 186

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13*->nLeeLdLsnN.LtslppglfsnLp<-* L+ L N+++++p++f+nL+

15088 187 ALQAMTLALNrISHIPDYAFQNLT 210

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019 *->nLeeLdLsnN.LtslppglfsnLp<-* +L+L+L+nN++++1 ++f++L

15088 211 SLVVLHLHNNrIQHLGTHSFEGLH 234

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2*->nLeeLdLsnN.LtslppglfsnLp<-* nLe+LdL++N+L+++p +++ L

15088 235 NLETLDLNYNKLQEFPV-AIRTLG 257

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11 *->nLeeLdLsnN.LtslppglfsnLp<-* +L+eL ++nN+++ +p+++f + p 15088 258 RLQELGFHNNnIKAIPEKAFMGNP 281

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32 *->nLeeLdLsnN.LtslppglfsnLp<-* L++++++N+++++++f+ Lp 15088 282 LLQTIHFYDNpIQFVGRSAFQYLP 305

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02*->nLeeLdLsnN..LtslppglfsnLp<-* +L++L+L++ +++++p+ +++++ 15088 306 KLHTLSLNGAmdIQEFPD--LKGTT 328

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52 *->nLeeLdLsnN.LtslppglfsnLp<-* +Le L L + +++ lp+g +++Lp 15088 329 SLEILTLTRAGIRLLPSGMCQQLP 352

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097*->nLeeLdLsnN.LtslppglfsnLp<-* +L++L Ls+N++++lp+ +++++ 15088 353 RLRVLELSHNqIEELPS--LHRCQ 374

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49 *->nLeeLdLsnN.LtslppglfsnLp<-* +Lee+ L++N++ ++ ++fs+L+

15088 375 KLEEIGLQHNrIWEIGADTFSQLS 398

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042*->nLeeLdLsnN.LtslppglfsnLp<-* +L+ LdLs N ++s++p++fs L 15088 399 SLQALDLSWNaIRSIHPEAFSTLH 422

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66*->nLeeLdLsnN.LtslppglfsnLp<-* +L +LdL +N+Lt+lp ++L

15088 423 SLVKLDLTDNqLTTLPLAGLGGLM 446 $7tm_1$: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2 *->dWpfGsalCklvtaldvvnmyaSillLta<-*

+W G ++C+ +++| v+ + aS+||Lt+ 15088 635 RWETG-LGCRATGFLAVLGSEASVLLLTL 662

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11 *->ICWIPyfivllIdtlc.lsiimsstCelervlptallvtlwLayvNs |+ P++++| ++ +++++++v|++ ++

15088 784 LLYCPVAFLSFASMLGIFPV------TPEAVKSVLLVVLPLPA 820

clNPilY<-* clNP++Y 15088 821 CLNPLLY 827

Searching for complete domains in SMART hmmpfam - search a single seq against HMM database HMMER 2.1.1 (Dec 1998) Copyright (C) 1992-1998 Washington University School of Medicine HMMER is freely distributed under the GNU General Public License (GPL). _____ /ddm/robison/smart/smart/smart.all.hmms HMM file: /prod/ddm/wspace/orfanal/oa-script.12184.seq Sequence file: ______ Query: 15088 Scores for sequence family classification (score includes all domains): E-value N Description 247.2 2.3e-70 14 LRR typ 2 1.8e-19 13 LRR_PS 2 78.1 33.5 4.9e-06 LRR_sd22_2 25.7 0.0011 lrrntl 3 11.8 LRR bac 2 7.7 4

LRR_RI_2						•		5.4
Parsed for	domains	:						
Model	Domain	seq-f	seq-t	hmm-f	hmm-t		score	E-value
lgrnt1	1/1	34	70	 1	38	[]	25.7	0.0011
LRR_PS_2	1/13	64	87	 1	24	[]	1.9	1.2e+02
LRR_typ_2	1/14	64	88	 1	24	[]	12.6	2.1
LRR bac 2	1/7	89	108	 1	20	[]	0.9	80
LRR PS 2	2/13	89	111	 1	24	[]	17.2	0.4
LRR typ 2	2/14	89	112		24			1.3e-05
LRR RI 2							3.6	
LRR bac 2	2/7	113	132	 1			1.6	
LRR PS 2						[]	1.1	1.5e+02
LRR_typ_2				 1		[]		0.1
LRR bac 2				 1	20	[]	0.1	1e+02
LRR PS 2			159	 1	24	[]	7.1	24
LRR typ 2				 1	24	[]	25.9	0.00095
LRR PS 2	5/13	161	183	 1	24	[]	11.4	6.6
LRR typ 2				 1	24	[]	27.5	0.00031
LRR sd22 2				 1	22	[]	5.3	31
LRR RI 2					28	[]	5.3	8
LRR PS 2					24	[]	7.0	25
LRR typ 2					24	[]	23.2	0.0062
LRR_PS_2								79
DIKK_10_2	7/14					11		0.0002

232 ..

LRR_typ_2 LRR_RI_2 3/4 235 .. 1 28 [] 1.2 31 209 3 13.5 22 [] LRR sd22_2 2/5 209 235 ... 10.7 4.1 252 .. LRR bac 2 4/7 233 20 [] 0.76 LRR_typ_2 LRR_PS_2 255 .. 1 24 [] 16.1 8/14 233 255 .. 17.1 0.43 24 [] 233 8/13 1e+02 20 [] 0.2 275 .. LRR_bac_2 5/7 256 1 85 24 [] 2.9 LRR PS 2 9/13 256 278 .. 1 0.0026 279 .. LRR_typ_2 9/14 256 24 [] 24.4 24 [] 3.1 29 327 350 .. 10/14 LRR_typ_2 1.3 370 .. 1 20 [] 14.6 LRR_bac_2 6/7 351 10.8 8 24 [] LRR PS 2 10/13 351 372 .. 1 LRR_sd22_2 LRR_typ_2 LRR_RI_2 7.6 16 351 372 .. 22 [] 3/5 24 [] 18.8 0.13 11/14 373 .. 351 19 378 .. 28 [] 2.6 4/4 351 1 24 [] 2.3 1e+02 LRR PS 2 11/13 373 396 .. 1 10 396 .. 6.8 12/14 374 24 [] LRR_typ_2 LRR_sd22_2 397 418 .. 1 22 [] 7.0 19 4/5 419 .. 24 [] 3.4 13.6 12/13 397 1 LRR PS 2 30.4 4.3e-05 24 [] LRR typ 2 13/14 397 420 .. 1 440 .. 18 421 1 20 [] 5.8 LRR bac 2 7/7 441 .. 22 [] 3.7 49 $LRR_sd2\overline{2}_2$ 5/5 421 442 .. 24 [] 5.5 39 LRR_PS_2 13/13 421 1 21.6 0.018 24 [] LRR_typ_2 14/14 421 444 .. 1

Alignments of top-scoring domains:

7/14

209

FIGURE 11

0.0002

28.1

24 []

```
lrrnt1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011
                   *->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<-*
                      +CPapC+C ++ ++ dCs++gL +vP dl + t +
                      ACPAPCHCQEdGIMLSADCSELGLS--AVPGDLDPLTAY
                                                                 70
       15088
LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02
                   *->LtsL.qvLdLsnNnLsGeIPsslgn<-*
                   L L+ +LdLs NnL+ e+ + 1+
                      LDPLtAYLDLSMNNLT-ELQPGLFH
       15088
LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
                   *->LpnL.reLdLsnNqLtsLPpgaFqg<-*
                      L L+ LdLs N+Lt+L pg+F++
                      LDPLtAYLDLSMNNLTELQPGLFHH
       15088
                64
LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
                   *->PpsLkeLnvsnNrLteLPeL<-*
                        +L+eL+ s+N+L+ P
       15088
                89
                      LRFLEELRLSGNHLSHIPGQ
LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+ L++L+Ls+N+Ls +IP + ++
                      LRFLEELRLSGNHLS-HIPGQAFS
       15088
                89
LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
                   *->LpnLreLdLsnNqLtşLPpgaFqg<-*
                      L+ L+eL+Ls+N+L+++P +aF+q
                                                  112
                      LRFLEELRLSGNHLSHIPGQAFSG
       15088
                89
LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
                   *->npsLreLdLsnNkl.gdeGaraLaeaLks<-*
                      ++ L+eL+Ls+N+l+++ G + ++L s
                      LRFLEELRLSGNHLSHIPG--QAFSGLYS
       15088
LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
                   *->PpsLkeLnvsnNrLteLPeL<-*
                        sLk+L +nN+L P+
               113
                      LYSLKILMLQNNQLGGIPAE
                                              132
       15088
LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L sL++L L+nN+L G + 1+
       15088
                      LYSLKILMLQNNQLGGIPAEALWE
               113
LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
                    *->LpnLreLdLsnNqLtsLPpgaFqg<-*</pre>
                      L +L+ L L+nNqL +P++a++
                      LYSLKILMLQNNQLGGIPAEALWE
       15088
               113
LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
                   *->PpsLkeLnvsnNrLteLPeL<-*
                       psL++L+ + N ++ Pe
                      LPSLQSLRLDANLISLVPER
       15088
               137
LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
                    *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+sLq+L+L N +s +P+ +
               137
                      LPSLQSLRLDANLIS-LVPERSFE
                                                  159
       15088
LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
                    *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      Lp+L++L+L+ N ++ +P++ F+g
                      LPSLQSLRLDANLISLVPERSFEG
       15088
               137
LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
                    *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+sL++L L +N L+ eIP
                      LSSLRHLWLDDNALT-EIPVRALN
               161
        15088
```

LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031

```
*->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      L++Lr+L L++N+Lt++P +a+++
                                                   184
                      LSSLRHLWLDDNALTEIPVRALNN
       15088
               161
LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
                   *->LtnLeeLdLsqNkI....kkiENLde<-*
                      L+ L++L+L +N +++ + + NL
                      LSSLRHLWLDDNALteipvRALNNLPA
       15088
               161
LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
                    *->npsLreLdLsnNklgdeGaraL..aeaLks<-*
                      ++sLr L+L +N 1++ +raL++ aL++
                      LSSLRHLWLDDNALTEIPVRALnnLPALQA
       15088
               161
LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
L+ Lq L+ N++s +IP+ ++
                      LPALQAMTLALNRIS-HIPDYAFQ
       15088
               185
LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062
                    *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      Lp+L+ L N++++P+ aFq+
                                                   208
               185
                      LPALQAMTLALNRISHIPDYAFQN
       15088
LRR_PS_2: domain 7 of 13, from 289 to 232: score 3.1, E = 79
                    *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      LtsL+vL+L+nN++
                                          s+
                      LTSLVVLHLHNNRIQHLGTHSFEG
                                                   232
               209.
       15088
LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002
                    *->LpnLreLdLsnNqLtsLPpgaFqg<-*</pre>
                       L++L +L+L+nN++++L
                      LTSLVVLHLHNNRIQHLGTHSFEG
                                                   232
        15088
               209
LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31
                    *->npsLreLdLsnNklgdeGaraLaeaLks<-*
                       ++sL +L+L nN + G + e+L+
                       LTSLVVLHLHNNRIQHLGTHSF-EGLHN
                209
        15088
LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
                    *->LtnLeeLdLsqNkI....kkiENLde<-*
                       Lt L++L L +N+I++ ++++E+L++
                       LTSLVVLHLHNNRIqhlgtHSFEGLHN
        15088
                209
 LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
                    *->PpsLkeLnvsnNrLteLPeL<-*
                        ++L++L+ ++N+L e+P
                                               252
        15088
                233
                       LHNLETLDLNYNKLQEFPVA
 LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1, E = 0.76
                    *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                       L+nL++LdL++N+L++P++
                                                    255
                       LHNLETLDLNYNKLQEFPVAI-RT
        15088
                233
 LRR_PS_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
                     *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                       L++L++LdL++N+L e+P +
                       LHNLETLDLNYNKLQ-EFPVAIRT
        15088
                233
 LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
                     *->PpsLkeLnvsnNrLteLPeL<-*
                         +L+eL+ nN+++ Pe
                        LGRLQELGFHNNNIKAIPEK
                 256
        15088
 LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85
                     *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                        L +Lq+L ++nNn+ IP+ +
                        LGRLQELGFHNNNIK-AIPEKAFM
                 256
         15088
 LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026
                     *->LpnLreLdLsnNqLtsLPpgaFqg<-*
```

```
L+ L+eL +nN++++P+ aF g
       15088
              256
                      LGRLOELGFHNNNI KAI PEKAFMG
LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      ++L+ L L + ++ LP+g++q
                      TTSLEILTLTRAGIRLLPSGMCQQ
       15088
               327
LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3
                  `'*->PpsLkeLnvsnNrLteLPeL<-*
                       p+L+ L s+N+++eLP L
                      LPRLRVLELSHNQIEELPSL
       15088
LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-
                      L++L+vL+Ls+N++ e+Ps l +
                      LPRLRVLELSHNQIE-ELPS-LHR
       15088
               351
LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
                   *->LtnLeeLdLsqNkIkkiENLde<-*
                      L +L++L+Ls+N+I+ + L+
                      LPRLRVLELSHNQIEELPSLHR
       15088
               351
LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      Lp Lr+L Ls+Nq+++LP + ++.
                      LPRLRVLELSHNQIEELP-SLHRC
       15088
               351
LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
                   *->npsLreLdLsnNklgdeGaraLaeaLks<-*
+p+Lr+L Ls+N + + + ++ L++
                      LPRLRVLELSHNQIEELPSLHRCQKLEE
     15088
               351
LRR PS 2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      +++L+++ L++N++
                                      +++++
                      CQKLEEIGLQHNRIWEIGADTFSQ
       15088
LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                        +L+e L++N++ ++ +++F+
                      -QKLEEIGLQHNRIWEIGADTFSQ
       15088
               374
LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19
                    *->LtnLeeLdLsqNkIkkiENLde<-*
                      L+ L+ LdLs+N I++i
               397
                      LSSLQALDLSWNAIRSIHPEAF
                                                 418
       15088
LRR_PS_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4
                    *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+sLq LdLs+N + +I ++ ++
                      LSSLQALDLSWNAIR-SIHPEAFS
       15088
               397
LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05
                    *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      L++L+ LdLs+N+++s++p+aF+
                      LSSLQALDLSWNAIRSIHPEAFST
       15088
               397
LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18
                    *->PpsLkeLnvsnNrLteLPeL<-*
                       +sL +L+ +N+Lt+LP
                       LHSLVKLDLTDNQLTTLPLA
                                               440
                421
       15088
LRR sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49
                    *->LtnLeeLdLsqNkIkkiENLde<-*
                      L+ L+ LdL +N+++ + L +
                       LHSLVKLDLTDNQLTTL-PLAG
       15088
                421
LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39
                    *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                       L+sL+ LdL +N+L+ ++P
```

LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018

->LpnLreLdLsnNqLtsLPpgaFqg<-
L++L +LdL +NqLt+LP ++g
15088 421 LHSLVKLDLTDNQLTTLPLAGLGG

15088

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GAP of: FrGcgManager_101_HTAUB3ha_ check: 2817 from: 1 to: 3637
mLGR6 - 1 (analysis only) - Import - complete
to: FrGcgManager_101_ITAOfLsO_ check: 3059 from: 1 to: 2711
corrected human LGR6 (analysis o - Import - complete
Symbol comparison table:
/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760
    Gap Weight: 12
Length Weight: 4
                         Average Match: 10.000
                       Average Mismatch: 0.000
                                        3688
         Quality: 21826
                                Length:
                                      20
           Ratio: 8.051
                                 Gaps:
Percent Similarity: 84.248 Percent Identity: 84.211
     Match display thresholds for the alignment(s):
               | = IDENTITY
                    5
FrGcgManager_101_HTAUB3ha_ x FrGcgManager_101_ITA0fLs0_
    901 CCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAACTAT 950
                                                    MOUSE
                 1 ......GGGCTGCACAATCTGGAGACACTAGACCTGAATTAT 36
                                                    HUMAN
    951 AATGAGCTGCAGGAGTTCCCCTTGGCTATCCGGACCCTGGGCAGACTGCA 1000
       37 AACAAGCTGCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCA 86
   1001 AGAATTGGGTTTCCATAACAACAACATCAAGGCTATCCCAGAGAAAGCCT 1050
        87 GGAACTGGGGTTCCATAACAACAACATCAAGGCCATCCCAGAAAAGGCCT 136
   1051 TCATGGGCAACCCTCTCCTGCAGACAATACATTTTTATGACAACCCAATC 1100
       137 TCATGGGGAACCCTCTGCTACAGACGATACACTTTTATGATAACCCAATC 186
   1101 CAGTTTGTGGGAAGGTCAGCATTCCAGTACCTGTCTAAACTGCATACGCT 1150
       187 CAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAAACTCCACACACT 236
   1151 ATCTTTGAATGGTGCCACTGATATCCAAGAGTTCCCAGACCTCAAAGGCA 1200
       237 ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGGCA 286
   1201 CCACTAGCCTGGAGATCCTGACCCTGACCCGTGCGGGCATCAGACTGCTC 1250
       287 CCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTC 336
   1251 CCACCGGGAGTGTGCCAACAGCTGCCTAGGCTCCGAATCCTGGAGCTGTC 1300
       337 CCATCGGGGATGTGCCAACAGCTGCCCAGGCTCCGAGTCCTGGAACTGTC 386
```

1301	TCATAATCAGATCGAGGAGTTACCCAGCCTGCACAGATGTCAGAAGCTGG	1350
387	TCACAATCAAATTGAGGAGCTGCCCAGCCTGCACAGGTGTCAGAAATTGG	436
1351	AGGAAATTGGCCTCCGACATAACAGGATCAAGGAAATTGGTGCAGATACC	1400
437	AGGAAATCGGCCTCCAACACCACCGCATCTGGGAAATTGGAGCTGACACC	486
1401	TTCAGCCAGCTGGGCTCCTTGCAAGCTTTAGACCTGAGTTGGAATGCCAT	1450
487	TTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCAT	536
1451	CCGTGCCATCCACCCTGAGGCTTTCTCAACCCTTCGATCCTTGGTTAAGC	1500
537	CCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACTCCCTGGTCAAGC	586
1501	TGGACCTGACAACCAGCTGACCACACTGCCCCTGGCTGGGCTGGGA	1550
587	TGGACCTGACAGCAGCTGACCACACTGCCCCTGGCTGGACTTGGG	636
1551	GGCCTGATGCACCTGAAGCTCAAAGGGAACTTGGCCCTGTCTCAGGCCTT	1600
637	GGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCCCAGGCCTT	686
1601	CTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCCTACGCCT	1650
687	CTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCT	736
1651	ACCAGTGCTGTGCCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCTGGG	1700
737	ACCAGTGCTGTCCCTATGGGATGTGTCCCAGCTTCTTCAAGGCCTCTGGG	786
1701	CAGTGGCAGGCCGAGGACTTTCATCCAGAAGAAGAGGAGGCACCAAAGAG	1750
787	CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAG	836
1751	GCCCCTGGGTCTCCTTGCTGGACAAGCTGAGAACCACTATGACCTAGACC	1800
837	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	886
1801	TGGATGAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCCAGTGTC	1850
887	TGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACCCCAGTGTC	936
1851	CAGTGCAGCCCTGTTCCAGGCCCCTTCAAGCCCTGCGAGCACCTCTTTGA	1900
937	$\begin{matrix} \text{CAGTGTAGCCCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGA} \\ \cdot & \cdot & \cdot & \cdot \end{matrix}$	986
1901	GAGCTGGGGCATCCGCCTTGCTGTGTGGGCCATCGTGCTCTCCGTAC	1950
	AAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGC	
1951	TCTGTAACGGGCTGGTGCTGACAGTCTTTGCCAGCGGACCCAGCCCG	
1037	$\begin{tabular}{lllllllllllllllllllllllllllllllllll$	
	CTGTCCCCGTCAAGCTTGTGGTGGGTGCGATGGCAGGCGCCAACGCCCT	
1097	CTCCCCCCCTCA $ACTTTCCTACCTACCCATTCCACCCCCAACACCCTT$	1136

	GACGGGCATTTCCTGTGGTCTCCTGGCCTCTGTGGACGCCTTGACCTATG	
2101	GTCAGTTCGCTGAGTATGGAGCCCGCTGGGAGAGCGGTCTGGGCTGCCAG	2150
1187	GTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGG	1236
2151	GCTACGGGCTTCCTGGCTGCTGGGTTCAGAGGCGTCGGTGCTGCT	2200
1237	GCCACTGGCTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCTGCT	1286
2201	CACACTGGCGGCCGTGCAGTGCAGCATCTCTGTGACCTGCGTCCGAGCCT	2250
1287	CACTCTGGCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCT	1336
2251	ACGGGAAGGCGCCGTCGCCTGGCAGCGTCCGCGCAGGCGCACTGGGATGC	2300
1337	ATGGGAAGTCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCCTAGGCTGC	1386
2301	CTGGCGCTGGCCGGGCTGGCCGCAGCACTGCCGCTGGCCTCGGTGGGAGA	2350
1387	CTGGCACTGGCAGGGCTGGCCGCACTGCCCTGGCCTCAGTGGGAGA	1436
2351	GTATGGCGCCTCCCCACTCTGCCTGCCCTACGCCCCACCCGAGGGCCGGC	2400
	ATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGGTCAGC	
	CGGCCGCCTGGGCTTCGCTGTAGCCCTGGTGATGAACTCGCTCTGC	
	CAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGATCCTTCTGT	
	TTCCTGGTGGTGGCCGGCCCTACATCAAGCTCTACTGTGACCTGCCACG	
	TTCCTGGTCGTGGCCGGTGCCTACATCAAACTGTACTGT	
	GGGTGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGCGCCACGTGGCCT	2550
	GGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCT	1636
		2600
1637	GGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGC	
	TTTGCCTCCATGCTGGGCCTCTTCCCTGTCACCCCCGAGGCTGTCAAGTC	
	TTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGTC	1736
	AGTCCTTCTGGTGGTGCTGCCTCTGCCTGCCTGCCTCAACCCACTGCTCT	
	TGTCCTGCTGGTGGTGCCCCTGCCTGCCTGCCTCAACCCACTGCTGT	1786
	ACCTGCTCTTCAACCCTCACTTCCGGGATGACCTTCGGCGGCTCTGGCCA	
	ACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGCCTTCGGCCC	
	AGCCCTCGGTCCCCAGGGCCCCTAGCCTACGCTGCAGCCGGTGAGCTGGA	
1027	CCCCCACCCCACTCACCCCCTACCCTATCCTGCGCCCGGGGAGCTGGA	1886

2801	GAAGAGCTCCTGCGACTCCACCCAAGCGCTGGTGGCTTTCTCAGATGTGG	2850
1887	GAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGG	1936
2851	ATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCCTGGGCTAGAGACC	2900
1937		1986
2901	TATGGCTTCCCTTCAGTGACCCTCATCTCCCGACATCAGCCGGGGGCCAC	2950
1987	TATGGCTTCCCCTCAGTGACCCTCATCTCCTGTCAGCAGCCAGGGGCCCC	2036
2951	CAGGCTGGAGGGAACCATTTTATAGAGTCTGATGGAACCAAGTTTGGGA	3000
2037	CAGGCTGGAGGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGA	2086
3001	ACCCACAACCTCCCATGAAGGGAGAACTGCTGCTGAAGGCAGAGGGAGCC	3050
2087	ACCCCCAACCCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCT	2136
3051	ACTTTGGCAGGCTGTGGCTCTTCCGTGGGTGGAGCCCTCTGGCCCTCTGG	3100
	ACGCCAGCAGGTGGAGGCTTGTCAGGGGGTGGCGGCTTTCAGCCCTCTGG	
3101	CTCTCTCTTTGCCTCTCACTTGTAAATATCCCT	3133
2187	CTTGGCCTTTGCTTCACACGTGTAAATATCCCTCCCCATTCTTCTCTCCC	2236
3134	.CTCTGTTTGTCCTCTCCCCATCCAATGATGGCTGCTTATAA	3174
	$\begin{matrix} \texttt{CCTCTCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAA} \\ \vdots & \vdots & \ddots & \vdots \\ \end{matrix}$	
3175	AAGAAAGACTCCAACTCCATAGCAAGATGGCCAAC	3212
2287	AACAAATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAG	2336
3213	ACCTCTGACTCCATTGTTCTCTCTCCACGACCCCTAACCAATGAGTG	3259
	TAC.CTGGCTCCACTGATCACCTCTCTCTGTGACCATCACCAACGGGTG	
	CTTCCAAGTCTTGCTTTGTCTTGGCCTTCAGCTTCACCTTTCACCCTG	
	CCTCTTGGCCTTGCCTTGGCCTTCACCTTGATACTG	
	GGCCTTCTCTGTCCAATCCAATACTTCTGA.CAGAGGCCTGGGAAATT	
	GGCCTCTTCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTT	
	TGCATAGGAGAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGC	
	GTCTGCTTAAGGGAAATGAGGGAAG.TAAAGACAGTGAAGGGG.	
	CCTGACAGAGCCATGATCAGTAAGTGCAGAGT.GATGGGGAGGTCTCACA	
	TGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACA	
	GAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCTG	
2569	GAGAAAGGC.CTGGAAGGTGATTTCCCGTGTGACTC	2603

3500	TGACATATAGAATATAAAATGTGTTCTGCGTTCCATTAATCTTGACCTAT	3549
2604	ATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATAT	2651
3550	GCTGNGCCAAAGTGCTTCCTGTTAAAATACACTTTGGAAGACATTGAAAA	3599
	11 :11 11 111111 1111111 111111 111111 111	
2652	GCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATTAAAAA	2701
3600	АААААААААААААААААААААААААAAGGGCGGCCGC 3637	
2702	ААААААААА	

FIGURE 12 CONT.

COCKET COCCETE

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GAP of: FrGcgManager_102_MTAOuXMaE check: 8470 from: 1 to: 968
mLGR6.aa (analysis only) - Import - complete
to: FrGcgManager_102_NTAf7nCl_ check: 5092 from: 1 to: 737
corrected hLGR6.aa (analysis onl - Import - complete
Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102
 Matrix made by matblas from blosum62.iij
                  12
       Gap Weight:
                         Average Match: 2.778
    Length Weight:
                      Average Mismatch: -2.248
         Quality:
                3424
                                Length: 968
          Ratio: 4.646
                                 Gaps:
Percent Similarity: 90.773 Percent Identity: 89.281
      Match display thresholds for the alignment(s):
               | = IDENTITY
FrGcgManager_102 MTA0uXMaE x FrGcgManager 102 NTAf7nCl
   201 IPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFP 250
                                                    MOUSE
                                1 ......GLHNLETLDLNYNKLQEFP 19
                                                    HUMAN
   251 LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
      20 VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 69
   301 FQYLSKLHTLSLNGATDIQEFPDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350
      70 FQYLPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ 119
   351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSOLGSL 400
      120 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 169
   401 QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
      170 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 219
   451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF 500
      220 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL 269
   501 HPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPG 550
      1 :: 11. 11111111 1111111 1111111: 11111.1111111 11
   270 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 319
   551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLV 600
```

320 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 369

601	VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV	650
370	VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV	419
651	LGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA	700
420	LGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLA	469
701	AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMMNSLCFLVVAGA	750
470	AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGA	519
751	YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL	800
520	YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL	569
801	FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGP	850
570		619
	LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT	900
		669
901	LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGS	950
670	LISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL	719
951	SVGGALWPSGSLFASHL* 968	
720	SGGGGFQPSGLAFASHV* 737	

FIGURE 13 CONT.

>15088

> Fbh150881 - Import - vector trimmed

CCGCCSGCGGTGCAGCCCGCCGGGACCGGGAGGCGGCAGCTGCGGCCACCGCGCCGTGCG TCCGCGCCCGGCCAGGTGCCCCAGTAGCCCGACCGCCGAGATGCCCAGCCCGCCGGG GCTCCGGGCGCTATGGCTTTGCGCCGCGCTGTGCGCTTCCCGGAGGGCCGGCGCGCCCCC CCAGCCCGGCCCGGGCCCACCGCCTGCCGGCCCCTGCCACTGCCAGGAGGACGGCAT CATGCTGTCTGCCGACTGCTCTGAGCTCGGGGCTGTCCGCCGTTCCGGGGGACCTGGACCC CCTGACGGCTTACCTGGACCTCAGCATGAACAACCTCACAGAGCTTCAGCCTGGCCTCTT CCACCACCTGCGCTTCTTGGAGGAGCTGCGTCTCTCTGGGAACCATCTCTCACACATCCC AGGACAAGCATTCTCTGGTCTCTACAGCCTGAAAATCCTGATGCTGCAGAACAATCAGCT GGGAGGAATCCCCGCAGAGGCGCTGTGGGAGCTGCCGAGCCTGCAGTCGCTGCGCCTAGA CCTCTGGCTGGACGACAATGCACTCACGGAGATCCCTGTCAGGGCCCTCAACAACCTCCC TGCCCTGCAGGCCATGACCCTGGCCCTCAACCGCATCAGCCACATCCCCGACTACGCGTT CCAGAATCTCACCAGCCTTGTGGTGCTGCATTTGCATAACAACCGCATCCAGCATCTGGG GACCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAATTATAACAAGCT GCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCAGGAACTGGGGTTCCATAA CAACAACATCAAGGCCATCCCAGAAAAGGCCTTCATGGGGAACCCTCTGCTACAGACGAT ACACTTTTATGATAACCCAATCCAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAA ACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGG CACCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGGG GATGTGCCAACAGCTGCCCAGGCTCCGAGTCCTGGAACTGTCTCACAATCAAATTGAGGA GCTGCCCAGCCTGCACAGGTGTCAGAAATTGGAGGAAATCGGCCTCCAACACAACCGCAT CTGGGAAATTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAG CTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACTCCCTGGTCAA GCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCAGGCCTTCTCCAAGGACAGTTTCCC AAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAGTGCTGTCCCTATGGGATGTGTGC CAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGA GTCTTCAAAAAGGCCCCTGGGCCTCCTTGCCAGACAAGCAGAAACCACTATGACCAGGA CCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAG CCCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCT GGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGGTGCTGACCGT GTTCGCTGGCGGGCCTGCCCCCTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGG CGCCAACACCTTGACTGGCATTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTT TGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGG CTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCTGCTCACTCTGGCCGCAGTGCA TCGAGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCACTGCCCCTGGC CTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGGTCA GCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACTCCTTCTGTTTCCTGGT CGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCGGGGCGACTTTGAGGCCGT GTGGGACTGCCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTA CTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGA GTACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCGCGCAGG GGACTCAGGGCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGCTCCTGTGATTC TACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTGGAAGCTTCTGAAGCTGG GCGGCCCCTGGGCTGGAGACCTATGGCTTCCCCTCAGTGACCCTCATCTCCTGTCAGCA GCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGG GAACCCCCAACCCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGC AGGTGGAGGCTTGTCAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACA GGTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCTATAGC GCCTCTTGGCCTGGCCTTCCCTCAGCTTCACCTTGATACTGGGCCTCTTC CTTGTCATGTCTGAAGCTGTGGACCARAGACCTGGACTTTTGTCTGCTTAAGGGAAATGA GGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCT CACARAAAAGGCCTGGAAGGKGATTTCCCGTGTGACTCATGGRTAGGAWACAAAATGTG TTCCATGTACCATTAATCTTGACATATGCCATGCATAAARACTTCCTATTAAAATAAGCT **TTGGRAGAGATT**

>15088
MPSPPGLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSADCSELGLSAVPGDLDPLTAYLDLSMNNLT
ELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS
SLRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSLVVLHLHNNRIQHLGTHSFEGLHNLETLDLNYNK
LQEFPVAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLPKLHTLSLNGAMDIQEFPDLKGTT
SLEILTLTRAGIRLLPSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSLQALDLSWNAIR
SIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASG
QWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYLFESWGIRLAVWAIVL
LSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSE
ASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQPAALGFTVA
LVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVL
PLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFP
SVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGLSGGGGFQPSGLAFASHV*

```
protein alignment between mouse and human
> LGR6.
15088m(analysis only) - Import - complete
to: FrGcgManager_9_QBAsD4iW_ check: 8637 from: 1 to: 968
15088h(analysis only) - Import - complete
Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102
 Matrix made by matblas from blosum62.iij
                          Average Match: 2.778
       Gap Weight:
                    12
                        Average Mismatch: -2.248
    Length Weight:
                 4495
                                         968
         Quality:
                                Length:
           Ratio: 4.653
                                  Gaps:
                                          2
Percent Similarity: 91.097
                        Percent Identity: 89.855
      Match display thresholds for the alignment(s):
               | = IDENTITY
                : =
                   2
FrGcgManager 9 PBA0KgkFJ x FrGcgManager 9 QBAsD4iW March 15, 19101 15:24
     1 MHSPPGLLALWLCAVLCASARGGSDPQPGPGRPACPAPCHCQEDGIMLSA 50
                                                   Mouse
       1 MPSPPGLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSA 50
                                                   Human
    51 DCSELGLSVVPADLDPLTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGN 100
       51 DCSELGLSAVPGDLDPLTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGN 100
   101 HLSHIPGOAFSGLHSLKILMLOSNOLRGIPAEALWELPSLQSLRLDANLI 150
       101 HLSHIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLI 150
   151 SLVPERSFEGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRH 200
       151 SLVPERSFEGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISH 200
   201 IPDYAFONLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFP 250
       201 IPDYAFQNLTSLVVLHLHNNRIQHLGTHNFEGLHNLEPLDLNYNKLQEFP 250
   251 LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
       251 VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
   301 FQYLSKLHTLSLNGATDIQEFPDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350
       301 FQYLPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ 350
```

FIGURE 16

351 351	LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL :	400
	OALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL	450
401		450
451 451	KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF	500 500
501		550
501	:: .	550
551	PFKPCEHLFESWGIRLAVWAIVLLSVLCNG.VLLTVFASGPSPLSP.KLV	598
551	: :	600
599	VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV	648
601	VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV	650
649 651	LGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA	698 700
		748 750
	YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL	798
749 751		800
799	FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGP	848
801		850
849	LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT	898
851		900
899	LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGS	948
901		950
949	SVGGALWPSGSLFASHL* 966	
951	SGGGGFQPSGLAFASHV* 968	